

```

1 MVRSGNKAADVLCMDVGFMTMSNIPGIESPFQAKKVITMFVQRQVFAEN 50
  |||||
1 MVRSGNKAADVLCMDVGFMTMSNIPGIESPFQAKKVITMFVQRQVFAEN 50

51 KDEIALVLFGTGTDNPLSGGDQYQNI TVHRHMLPDPFDLLEDIESKIOP 100
  |||||
51 KDEIALVLFGTGTDNPLSGGDQYQNI TVHRHMLPDPFDLLEDIESKIOP 100

101 GSQQADFELDALIVSMDVIQHETIGKKFEKRHIEIFTDLSSRFSKSQLDII 150
  |||||
101 GSQQADFELDALIVSMDVIQHETIGKKFEKRHIEIFTDLSSRFSKSQLDII 150

151 IHSLKKCDISLQFFLPFSLGKEDGSGDRGDPFRLGGHGPSFPLKGITEQ 200
  |||||
151 IHSLKKCDISLQFFLPFSLGKEDGSGDRGDPFRLGGHGPSFPLKGITEQ 200

201 QKEGLEIVKMVMISLEGEDGLDEIYSFSESLRKL CVFKKIERHSIHWPCR 250
  |||||
201 QKEGLEIVKMVMISLEGEDGLDEIYSFSESLRKL CVFKKIERHSIHWPCR 250

```

Fig. 1

251 LTIGSNLSIRIAAYKSILQERVKKTWTVVDAKTLKKEDIQKETVYCLNDD 300
 |||||
 251 LTIGSNLSIRIAAYKSILQERVKKTWTVVDAKTLKKEDIQKETVYCLNDD 300
 .
 301 DETEVLKEDI IQFRYGS DIVPFSKVDEEQMKYKSEGKCFSVLGFCKSSQ 350
 |||||
 301 DETEVLKEDI IQFRYGS DIVPFSKVDEEQMKYKSEGKCFSVLGFCKSSQ 350
 .
 351 VQRRFFMGNOVLKVFAARDDEAAVALSSLIHALDDLDMVAIVRYAYDKR 400
 |||||
 351 VQRRFFMGNOVLKVFAARDDEAAVALSSLIHALDDLDMVAIVRYAYDKR 400
 .
 401 ANPQVGVAFPHIKHNYECLVYVQLPFMEDLRQYMFSSLNKSKKYAPTEAQ 450
 |||||
 401 ANPQVGVAFPHIKHNYECLVYVQLPFMEDLRQYMFSSLNKSKKYAPTEAQ 450
 .
 451 LNAVDALIDMSLAKKDEKTDLTLEDLPFTTKIPNPRFQRLFQ 492
 |||||
 451 LNAVDALIDMSLAKKDEKTDLTLEDLPFTTKIPNPRFQRLFQ 492

Fig. 1 (Cont.)

[illegible]

Fig. 2.

```

251 LTIGSNLSIRIAAYKSILQERVKKTWTVVDAKTLKKEDIQKETVYCLNDD 300
|||||
251 LTIGSNLSIRIAAYKSILQERVKKTWTVVDAKTLKKEDIQKETVYCLNDD 300
.
301 DETE..... 304
||||
301 DETEVLKEDIQGFYGSDIVPFSKVDEEQMKYKSEKCFSVLGFCKSSQ 350
.
305 .....LNPPAEVTTKSQIPLSKIKTLFPLIEAKKKDQVTA 339
|||||
501 PREPLPPIQQHIWNMLNPPAEVTTKSQIPLSKIKTLFPLIEAKKKDQVTA 550
.
340 QEIFQDNHEDGPTAKKCLKTEQGAHFSVSSLAEGSVTSVGSVNPAENFRV 389
|||||
551 QEIFQDNHEDGPTAKKCLKTEQGAHFSVSSLAEGSVTSVGSVNPAENFRV 600
.
390 LVKQKKASFEESASNLINHIEQFLDTNETPYFMKSIDCIRAFREEAIFKS 439
|||||
601 LVKQKKASFEESASNLINHIEQFLDTNETPYFMKSIDCIRAFREEAIFKS 650

```

Fig. 2 (Cont.)

```

440 EEQRFNNFLKALQEKVEIKQLNHFWEIVVQDGITLITKEEASGSSVTAAE 489
    |||||
651 EEQRFNNFLKALQEKVEIKQLNHFWEIVVQDGITLITKEEASGSSVTAAE 700
    |||||

    490 AKKFLAPKDKPSGDTAAVFEEGGDVDDLDMI 521
        |||||
    701 AKKFLAPKDKPSGDTAAVFEEGGDVDDLDMI 732

```

Fig. 2 (Cont.)

2 GCGCSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIRNGSEVRDPLVTY 51
 |||||
 1 GCGCSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIRNGSEVRDPLVTY 50
 52 EGSNPPASPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQ 101
 |||||
 51 EGSNPPASPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQ 100
 102 SLTTGQEGFIPNFVAKANSLEPEPWFVKNSRKDAERQLLAPGNTHGSF 151
 |||||
 101 SLTTGQEGFIPNFVAKANSLEPEPWFVKNSRKDAERQLLAPGNTHGSF 150
 152 LIRESESTAGSFSLSVRDFDQNGEVVKHYKIRNLDNGGFYISPRITFP 201
 |||||
 151 LIRESESTAGSFSLSVRDFDQNGEVVKHYKIRNLDNGGFYISPRITFP 200
 202 LHELVRHYTNASDGLCTRLSRPCQTQKPQKPWWEDEWEVPRETCLKLVERL 251
 |||||
 201 LHELVRHYTNASDGLCTRLSRPCQTQKPQKPWWEDEWEVPRETCLKLVERL 250

Fig. 3

```

252 GAGQGEVWMGYNGHTKVAVKS LKQGS MSPDAFLAEANL MKQLQHRLV 301
      |||||
251 GAGQGEVWMGYNGHTKVAVKS LKQGS MSPDAFLAEANL MKQLQHRLV 300
      |||||

302 RLYAVVTQEPIYIITEYMENGLVDFL KTPSGIKLTINKLLDMAAQIAEG 351
      |||||
301 RLYAVVTQEPIYIITEYMENGLVDFL KTPSGIKLTINKLLDMAAQIAEG 350

352 MAFIEERNYIHRDLRAANILVSDTL SCKIADFGLARLIEDIHHQVR 397
      |||||
351 MAFIEERNYIHRDLRAANILVSDTL SCKIADFGLARLIEDNEYTAR 396

```

Fig. 3(Cont.)

```

302 TLKLVERLGAGQFGEVWMGYNGHTKVAVKSLKQGSMSPD AFLAEANL MK 351
|||||
243 TLKLVERLGAGQFGEVWMGYNGHTKVAVKSLKQGSMSPD AFLAEANL MK 292

352 QLQHRLVRLYAVVTOEPIYII TEYMENGSLVD FLKTPSGIKLTINKLLD 401
|||||
293 QLQHRLVRLYAVVTOEPIYII TEYMENGSLVD FLKTPSGIKLTINKLLD 342

402 MAAQIAEGMAFIEERNYIHRDLRAANILVSDTL SCKIADEGLARLIEDNE 451
|||||
343 MAAQIAEGMAFIEERNYIHRDLRAANILVSDTL SCKIADEGLARLIEDNE 392

452 YTAREGAKFPIKWTAPEAINYGTTIKSDVWSFGILLTEIVTHGRIPYPG 501
|||||
393 YTAREGAKFPIKWTAPEAINYGTTIKSDVWSFGILLTEIVTHGRIPYPG 442

502 MTNPEVIQNLERGYRMVRPDNCPEELYQLMRLC WKERPEDRPTFDYLR SV 551
|||||
443 MTNPEVIQNLERGYRMVRPDNCPEELYQLMRLC WKERPEDRPTFDYLR SV 492

552 LEDFFTATEGQYQPQP 567
|||||
493 LEDFFTATEGQYQPQP 508

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Fig. 4 (Cont.)


```

2 GCGCSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIRNGSEVRDPLVTY 51
  |||||
1 GCGCSSHPEDDWMENIDVCENCHYPIVPLDGKGTLLIRNGSEVRDPLVTY 50
52 EGSNPPASPLQGDPQQGLKDKACGSLAVGFHLSPTYFLPGLAFLVPHPV 101
  |||||
51 EGSNPPASPLQ..... 61

102 TPGFLPIPARFSLTPLVFTDNLVIALHSYEPSHGDGLGFEKGEQLRILEQ 151
  |||||
62 .....DNLVIALHSYEPSHGDGLGFEKGEQLRILEQ 92

152 SGEWWKAQSLTTGQEGFIPFNFAKANSLPEPEWFFKNLSRKDAERQLLA 201
  |||||
93 SGEWWKAQSLTTGQEGFIPFNFAKANSLPEPEWFFKNLSRKDAERQLLA 142

202 PGNTHGSFLIRESESTAGSFLSVRDFDQNGGEVVKHYKIRNLDNGGFYI 251
  |||||
143 PGNTHGSFLIRESESTAGSFLSVRDFDQNGGEVVKHYKIRNLDNGGFYI 192

252 SPRITFPGLHELVRHYTNASDGLCTRLSRPCQTQKPKPWWEDEWEVPRE 301
  |||||
193 SPRITFPGLHELVRHYTNASDGLCTRLSRPCQTQKPKPWWEDEWEVPRE 242

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Fig. 4

[illegible]

Fig. 5

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62 AEAIPCTLAVSNPHTDAWKSHGLVEVASYCEESRGNQWVPYISLQER 109
    | : | | . | | | | | | | | | | | | | | | | | | | | | | |
114 ARDLHC.LLVTNPHTDAWKSHGLVEVASYCEESRGNQWVPYISLQER 160

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Fig. 6

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1 MRARPQVCEALLFALALQGTVCYGIKWIALSKTPSALALNQTHCKQLEG 50
  |||||
1 MRARPQVCEALLFALALQGTVCYGIKWIALSKTPSALALNQTHCKQLEG 50

51 LVSAQVQLCRSNLELMHTVVHAAREVMKACRRAFADMRWNCSSIELAPNY 100
  |||||
51 LVSAQVQLCRSNLELMHTVVHAAREVMKACRRAFADMRWNCSSIELAPNY 100

101 LLDLERTRESAFVYALSAAISHAIACTSGDLPGCSCGPVGEPPGP 150
  |||||
101 LLDLERTRESAFVYALSAAISHAIACTSGDLPGCSCGPVGEPPGP 150

151 GNRWGRCADNLSYGLLMGAKFSDAPMKVKKTGSQANKLMRLHNSEVGRQA 200
  |||||
151 GNRWGRCADNLSYGLLMGAKFSDAPMKVKKTGSQANKLMRLHNSEVGRQA 200

201 LRASLEMKCKCHGVSGCSIRTCWKGLQELQDVAADLKTRYLSATKVVHR 250
  |||||
201 LRASLEMKCKCHGVSGCSIRTCWKGLQELQDVAADLKTRYLSATKVVHR 250

```

Fig. 7

251 PMGTRKHLVPKDLDIRPVKDSELVYLQSSPFCMKNEKVGSHGTQDRQCN 300
 |||||
 251 PMGTRKHLVPKDLDIRPVKDSELVYLQSSPFCMKNEKVGSHGTQDRQCN 300
 |||||
 301 KTSNGSDSCDLM.....CCYVTCRRCERTVER 327
 |||||
 301 KTSNGSDSCDLMCCGRGYNPYTDRVVERCHCKYHWCCYVTCRRCERTVER 350
 |||||
 328 YVCK 331
 ||||
 351 YVCK 354

Fig. 7 (Cont.)

1	MRARPQVCEALLFALALQTGVCYGIKWLALSKTPSALALNQTQHCKQLEG	50
1	MRARPQVCEALLFALALQTGVCYGIKWLALSKTPSALALNQTQHCKQLEG	50
51	LVSAQVQLCRSNLELMHTVVHAAREVMKACRRAFADMRWNCSSIELAPNY	100
51	LVSAQVQLCRSNLELMHTVVHAAREVMKACRRAFADMRWNCSSIELAPNY	100
101	LLDLERGTRSAFVYA.....	116
101	LLDLERGTRSAFVYALSAAATISHAIARACTSGDLPGCSCGPVGPPEPPGP	150
117AADLKTRYLSATKVVHR	133
201	LRASLEMKCKCHGVSGSCSIRTCWKGLQELQDVAADLKTRYLSATKVVHR	250
134	PMGTRKHLVPKDLDIRPVKDSELVYLQSSPDFCMKNEKVGSHGTQDRQCN	183
251	PMGTRKHLVPKDLDIRPVKDSELVYLQSSPDFCMKNEKVGSHGTQDRQCN	300

Fig. 8

184 KTSNGSDSCDLMCCGRGYNPYTDRVVERCHCKYHWCCYVTCRRCERTVER 233
|||||
301 KTSNGSDSCDLMCCGRGYNPYTDRVVERCHCKYHWCCYVTCRRCERTVER 350

234 YVCK 237

||||

351 YVCK 354

Fig. 8 (Cont.)

1 MSPFLRIGLSNFDGSCQSCQGEAVNPYCAVLVKEYVESENGQMYIQKKP 50
 |||
 1 MSPFLRIGLSNFDGSCQSCQGEAVNPYCAVLVKEYVESENGQMYIQKKP 50

51 TMYPPWDSTFDAHINKGRVMQIIVKGNVDLISSETVELYSLAERCCKNN 100
 |||
 51 TMYPPWDSTFDAHINKGRVMQIIVKGNVDLISSETVELYSLAERCCKNN 100

101 GKTEIWLELKPQGRMLMNARYFLEMSDTKDMNEFEFTEGFFALHQRRAIK 150
 |||
 101 GKTEIWLELKPQGRMLMNARYFLEMSDTKDMNEFEFTEGFFALHQRRAIK 150

151 QAKVHHVKCHEFTATFFPQPTFCVSCHEFVWGLNKQGYQCRQCNAAIHK 200
 |||
 151 QAKVHHVKCHEFTATFFPQPTFCVSCHEFVWGLNKQGYQCRQCNAAIHK 200

201 CIDKVIKCTGSAINSRSTMFKERFKIDMPHRFKVYNYKSPTFCEHCGT 250
 |||
 201 CIDKVIKCTGSAINSRSTMFKERFKIDMPHRFKVYNYKSPTFCEHCGT 250

251 LLWGLARQGLKCDACGMNVHHRQCQTKVANLCCGINQKLMAEALAMIESTQQ 300
 |||
 251 LLWGLARQGLKCDACGMNVHHRQCQTKVANLCCGINQKLMAEALAMIESTQQ 300

Fig. 9


```

301 ARCLRDTEQIFREGPVEIGLPCSIKNEARPPCLPTPGKREPQGISWESPL 350
|||||
301 ARCLRDTEQIFREGPVEIGLPCSIKNEARLPCLPTPGKREPQGISWESPL 350

351 DEVDKMCHLPEPELNKERPSLQIKLKIEDFILHKMLGKSGFKVFLAEFK 400
|||||
351 DEVDKMCHLPEPELNKERPSLQIKLKIEDFILHKMLGKSGFKVFLAEFK 400

401 KTNQFFAIKALKKDVVLMDDDVECTMVEKRVLSLAWEHFPLTHMECTFQT 450
|||||
401 KTNQFFAIKALKKDVVLMDDDVECTMVEKRVLSLAWEHFPLTHMECTFQT 450

451 KENLFFVMEYLNCGDLMYHIQSKHFDLSRATFYAAEIIILGLQFLHSGKI 500
|||||
451 KENLFFVMEYLNCGDLMYHIQSKHFDLSRATFYAAEIIILGLQFLHSGKI 500

501 VYRDLKLDNILLDKDGHIKIADFGMCKENMLGDAKTNTFCGTPDYIAPEI 550
|||||
501 VYRDLKLDNILLDKDGHIKIADFGMCKENMLGDAKTNTFCGTPDYIAPEI 550

```

Fig. 9 (Cont.)

551 LLGQKYNHSVDWWSFGVLLYEMLIQSPFHGQDEEEELFHSIRMDNPFYPR 600
 |||||
 551 LLGQKYNHSVDWWSFGVLLYEMLIQSPFHGQDEEEELFHSIRMDNPFYPR 600

601 WLEKEAKDLLVKV 613
 |||||
 601 WLEKEAKDLLVKL 613

Fig. 9(Cont.)

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1  MPI TRMRP WLEMQINSNQIPGLIWINKEEMIFQIPWKHAAKHGWDINK 50
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
1  MPI TRMRP WLEMQINSNQIPGLIWINKEEMILEIPWKHAAKHGWDINK 50
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
51 DACLFERSWAIHTGRYKAGEKEPDPKTWKANFR CAMNSLPDIEEVKDQSRN 100
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
51 DACLFERSWAIHTGRYKAGEKEPDPKTWKANFR CAMNSLPDIEEVKDQSRN 100
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
101 KGSSAVRVYRMLPPLTKNQKERRKSKSSRDAKSKAKRKSCGDSPTFSD 150
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
101 KGSSAVRVYRMLPPLTKNQKERRKSKSSRDAKSKAKRKSCGDSPTFSD 150
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
151 GLSSSTLPDDHSSYTVPGYMQDLEVEQALTPALSPCAVSS TLPDWHIPVE 200
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
151 GLSSSTLPDDHSSYTVPGYMQDLEVEQALTPALSPCAVSS TLPDWHIPVE 200
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
201 VVPDSTSDLYNFQVSPMPSTSEAT TDEDEEGKLPEDIMK LLEQSEWQPTN 250
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
201 VVPDSTSDLYNFQVSPMPSTSEAT TDEDEEGKLPEDIMK LLEQSEWQPTN 250
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
251 VDCKGYLLNEPGVQPTSVYGD FSCKEEPEIDSPGG 285
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
251 VDGKGYLLNEPGVQPTSVYGD FSCKEEPEIDSPGG 285
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||

```

Fig. 10

```

1 MWSWKCLLFWAVLVTATLCTARPSPTLPEQAQPWGAPVEVESFLVHPGDL 50
  |||||
1 MWSWKCLLFWAVLVTATLCTARPSPTLPEQAQPWGAPVEVESFLVHPGDL 50

51 LQLRCRLRDDVQSINWLRDGVQLAESNRTRITGEEVEVQDSVPADSGLYA 100
  |||||
51 LQLRCRLRDDVQSINWLRDGVQLAESNRTRITGEEVEVQDSVPADSGLYA 100

101 CVTSSPSGSDTTYFSVNVSDALPSSDDDDSSSEEKETDNTKPNRMP 150
  |||||
101 CVTSSPSGSDTTYFSVNVSDALPSSDDDDSSSEEKETDNTKPNRMP 150

151 VAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPD 200
  |||||
151 VAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPD 200

201 HRIGGYKVRyatWSIIMDSVVPsDKGNyTCIVENEyGSINHTYQLDVVER 250
  |||||
201 HRIGGYKVRyatWSIIMDSVVPsDKGNyTCIVENEyGSINHTYQLDVVER 250

251 SPHRPILQAGLPANKTVALGSNVFEFMCKVYSDPQPFIQWLKHIEVNGSKI 300
  |||||
251 SPHRPILQAGLPANKTVALGSNVFEFMCKVYSDPQPFIQWLKHIEVNGSKI 300

```

Fig. 11

```

301 GPDNLPYVQILKTAGVNTTDKEMEVHLHNRVSEFEDAGEYTCLAGNSIGLS 350
|||||
301 GPDNLPYVQILKTAGVNTTDKEMEVHLHNRVSEFEDAGEYTCLAGNSIGLS 350

351 HHSAWLTVLEALEERPAMVTSPLYLEIIIIYCTGAFLISCMVGSVIVYKMK 400
|||||
351 HHSAWLTVLEALEERPAMVTSPLYLEIIIIYCTGAFLISCMVGSVIVYKMK 400

401 SGTKKSDFHQSOMAVHKLAKSIPLRRQVTVSADSSASMSNGVLLVRPSRLS 450
|||||
401 SGTKKSDFHQSOMAVHKLAKSIPLRRQVTVSADSSASMSNGVLLVRPSRLS 450

451 SSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAI GL 500
|||||
451 SSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAI GL 500

501 DKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMI GKHKNIINLLGA 550
|||||
501 DKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMI GKHKNIINLLGA 550

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Fig. 11 (Cont.)

```

551 CTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQSSKDL 600
|||||
551 CTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQSSKDL 600
|||||
601 VSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADEGLARDIHH 650
|||||
601 VSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADEGLARDIHH 650
|||||
651 IDYKKTTNGRLPVKWMapealeFDRIYTHQSDVWSFGV 688
|||||
651 IDYKKTTNGRLPVKWMapealeFDRIYTHQSDVWSFGV 688

```

Fig. 11(Cont.)

2 PKRGKKGAVAE D G D E L R T E P E A K K S K T A A K K N D K E A A G E G P A L Y E D P P D Q 51
 |||||
 1 PKRGKKGAVAE D G D E L R T E P E A K K S K T A A K K N D K E A A G E G P A L Y E D P P D Q 50
 .
 52 K T S P S G K P A T L K I C S W N V D G L R A W I K K K G L D W V K E E A P D I L C L Q E T K C S E 101
 |||||
 51 K T S P S G K P A T L K I C S W N V D G L R A W I K K K G L D W V K E E A P D I L C L Q E T K C S E 100
 .
 102 N K L P A E L Q E L P G L S H Q Y W S A P S D K E G Y S G V G L L S R Q C P L K V S Y G I 146
 |||||
 101 N K L P A E L Q E L P G L S H Q Y W S A P S D K E G Y S G V G L L S R Q C P L K V S Y G I G D E E H 150
 .
 147 A Y V P N A G R G L V R L E Y R Q R W D E A F R K F L K G L A S 178
 |||||
 151 D Q E G R V I V A E F D S F V L V T A Y V P N A G R G L V R L E Y R Q R W D E A F R K F L K G L A S 200
 .
 179 R K P L V L C G D L N V A H E E I D L R N P K G N K K N A G F T P Q E R Q G F G E L L Q A V P L A D 228
 |||||
 201 R K P L V L C G D L N V A H E E I D L R N P K G N K K N A G F T P Q E R Q G F G E L L Q A V P L A D 250

Fig. 12

229 SERHLYPNTPYAYTFWTYMMNARSKNVGWRLDYFLLSHSLPALCDSKIR 300
|||||

251 SERHLYPNTPYAYTFWTYMMNARSKNVGWRLDYFLLSHSLPALCDSKIR 278
279 SKALGSDHCPITLYLAL 295
||||| 317
301 SKALGSDHCPITLYLAL

Fig. 12(Cont.)

2 PKRGKKGAVAE D G D E L R T G K G M K S A L L P R N C G G V C H S L D V R E P E A K K S K 51
 |||||
 1 PKRGKKGAVAE D G D E L R TE P E A K K S K 26

52 T A A K K N D K E A G E G P A L Y E D P P D Q K T S P S G K P A T L K I C S W N V D G L R A W I K 101
 |||||
 27 T A A K K N D K E A G E G P A L Y E D P P D Q K T S P S G K P A T L K I C S W N V D G L R A W I K 76

102 K K G L D W V K E E A P D I L C L Q E T K C S E N K L P A E L Q E L P G L S H Q Y W S A P S D K E G 151
 |||||
 77 K K G L D W V K E E A P D I L C L Q E T K C S E N K L P A E L Q E L P G L S H Q Y W S A P S D K E G 126

152 Y S G V G L L S R Q C P L K V S Y G I G D E E H D Q E G R V I V A E F D S F V L V T A Y V P N A G R 201
 |||||
 127 Y S G V G L L S R Q C P L K V S Y G I G D E E H D Q E G R V I V A E F D S F V L V T A Y V P N A G R 176

202 G L V R L E Y R Q R W D E A F R K F L K G L A S R K P L V L C G D L N V A H E E I D L R N P K G N K 251
 |||||
 177 G L V R L E Y R Q R W D E A F R K F L K G L A S R K P L V L C G D L N V A H E E I D L R N P K G N K 226

Fig. 13

252 KNAGFTPQERQGFCELLQAVPLADSEFRHLYPNTPYAYTFWTYMMNARSKN 301
 |||||
 227 KNAGFTPQERQGFCELLQAVPLADSEFRHLYPNTPYAYTFWTYMMNARSKN 276
 302 VGWRLDYFLLSHSLLPALCDSKIRSKALGSDHCPIITLYLAL 342
 |||||
 277 VGWRLDYFLLSHSLLPALCDSKIRSKALGSDHCPIITLYLAL 317

Fig. 13(Cont.)

1 MFQAAERPQEWAMEGPRDGLKKERLLDDRHSGLDSMKDEEYEQMVKELQ 50
 |||||
 1 MFQAAERPQEWAMEGPRDGLKKERLLDDRHSGLDSMKDEEYEQMVKELQ 50
 |||||
 1 MFQAAERPQEWAMEGPRDGLKKERLLDDRHSGLDSMKDEEYEQMVKELQ 100
 |||||
 51 EIRLEPQEVPRGSEPWKQQLTEDGDSFLHLAIIHEEKALTMENVIRQVKGD 100
 |||||
 51 EIRLEPQEVPRGSEPWKQQLTEDGDSFLHLAIIHEEKALTMENVIRQVKGD 150
 |||||
 101 LAFLNFQNNLQQTPHLAVITNQPEIAEALLGAGCDPELDRFRGNTPLHL 150
 |||||
 101 LAFLNFQNNLQQTPHLAVITNQPEIAEALLGAGCDPELDRFRGNTPLHL 200
 |||||
 151 ACEQGCLASVGVLTQSCCTPHLSILKATNYNGHTCLHLASIHGYLGIVE 200
 |||||
 151 ACEQGCLASVGVLTQSCCTPHLSILKATNYNGHTCLHLASIHGYLGIVE 250
 |||||
 201 LLVSLGADVNAQEPNCNGRTALHLAVDLQNPDLVSLLLKCGADVNRVTYQG 250
 |||||
 201 LLVSLGADVNAQEPNCNGRTALHLAVDLQNPDLVSLLLKCGADVNRVTYQG 250

Fig. 14

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251 YSPYQLTWGRPSTRIQQQLGQLTLLENLQMLPESEDEESYDTESEFFTE 300
      |||||
251 YSPYQLTWGRPSTRIQQQLGQLTLLENLQMLPESEDEESYDTESEFFTE 300

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Fig. 14 (Cont.)

1 MFQAAERPQEWAMEGPKDGLL..... 50
 1 MFQAAERPQEWAMEGPRDGLKKERLLDDRHDSGLDSMKDEEYEQMVKELO 50
 51 EIRLEPQEVPRGSEPWKQQLTEDGDSFLHLAIHHEEKALTMENVIRQVKGD 100
 51 EIRLEPQEVPRGSEPWKQQLTEDGDSFLHLAIHHEEKALTMENVIRQVKGD 100
 51 EIRLEPQEVPRGSEPWKQQLTEDGDSFLHLAIHHEEKALTMENVIRQVKGD 150
 101 LAFLNFQNNLQQTPHLAVITNQPEIAEALLGAGCDPELRDFRGNTPLHL 150
 101 LAFLNFQNNLQQTPHLAVITNQPEIAEALLGAGCDPELRDFRGNTPLHL 183
 151 ACEQGCLASVGLTQSCCTTPHLHSILKATNYNG..... 200
 151 ACEQGCLASVGLTQSCCTTPHLHSILKATNYNGHTCLHLASIHGYLGIVE 222
 184QEPCNGRTALHLAVDLQNPDLVSLLLKCGADVNRVTYQG 250
 201 LLVSLGADVNAQEPCNGRTALHLAVDLQNPDLVSLLLKCGADVNRVTYQG 250

Fig. 15

```

223 YSPYQLTWGRPSTRIQQQLTLENLQMLPESEDEESYDTESEFFTE 272
    |||||
251 YSPYQLTWGRPSTRIQQQLTLENLQMLPESEDEESYDTESEFFTE 300
    |||||

273 DELPYDDCVFGGQRLTL 289
    |||||
301 DELPYDDCVFGGQRLTL 317

```

Fig. 15 (Cont.)

```

1  MAGIFYFALFSCFGICDAVTGSRVYPANEVTLDSRSVQGELGWIASPL 50
  |||||
1  MAGIFYFALFSCFGICDAVTGSRVYPANEVTLDSRSVQGELGWIASPL 50

51  EGGWEEVSIMDEKNTPIRTYQVCNVMPEPSONNWLRTDWITREGAQRVYIE 100
  |||||
51  EGGWEEVSIMDEKNTPIRTYQVCNVMPEPSONNWLRTDWITREGAQRVYIE 100

101 IKFTLRDCNSLPGVMGTCKETFNLYYESDNDKERFIRENFVKIDTIAA 150
  |||||
101 IKFTLRDCNSLPGVMGTCKETFNLYYESDNDKERFIRENFVKIDTIAA 150

151 DESFTQVDIGDRIMKLNTEIRDVGPLSKKGFYLAQDVGACIALVSRVF 200
  |||||
151 DESFTQVDIGDRIMKLNTEIRDVGPLSKKGFYLAQDVGACIALVSRVF 200

201 YKKCPLTVRNLAQFPDITIGADTSSLVEVRGSCVNNSEEKDVPKMYCGAD 250
  |||||
201 YKKCPLTVRNLAQFPDITIGADTSSLVEVRGSCVNNSEEKDVPKMYCGAD 250

251 GEWLVPIGNCLCNAGHEERSGECQACKIGYYKALSTDAKCPPHSV 300
  |||||
251 GEWLVPIGNCLCNAGHEERSGECQACKIGYYKALSTDAKCPPHSV 300

```

Fig. 16

Fig. 16 (Cont.)

601 TYEDPNQAVREFAKEIDASCIEKIEKIVGVGEFGEVCSGRLKVP GKREICV 650
 |||||
 601 TYEDPNQAVREFAKEIDASCIEKIEKIVGVGEFGEVCSGRLKVP GKREICV 650
 651 AIKTLKAGYTDKQRRDFLSEASIMQFDHPNIIHLEGVVTKCKPVMIIITE 700
 |||||
 651 AIKTLKAGYTDKQRRDFLSEASIMQFDHPNIIHLEGVVTKCKPVMIIITE 700
 701 YMENGSLDAFLRKNDGRFTVIQLVGMRLRGISGMKYLSDMSYVHRDLAAR 750
 |||||
 701 YMENGSLDAFLRKNDGRFTVIQLVGMRLRGISGMKYLSDMSYVHRDLAAR 750
 751 NILVNSNLVCKVSDFGMSRVLEDDPEAAATTTRGGKIPIRWTAP EAIAYRK 800
 |||||
 751 NILVNSNLVCKVSDFGMSRVLEDDPEAAATTTRGGKIPIRWTAP EAIAYRK 800
 801 FTSASDVWSYGI VMWEVMSYGERPYWDM SNQD..... 832
 |||||
 801 FTSASDVWSYGI VMWEVMSYGERPYWDM SNQDV IKAIEEGYRLPPPMDCP 850
 833 PNT 835
 |||
 851 IALHQMLDCWQKERSDRPKFGQIVNMLDKLIRNPNSLKR TGT ESSRPNT 900

Fig. 16(Cont.)

836 ALLDPSSPEFSAVSVGDWLQAIKMDRYKDNE "LAA G I L L E A V A T T E R
901 ALLDPSSPEFSAVSVGDWLQAIKMDRYKDNETAAGYTTLEAVVHVNOED 950

886 LARIGITAITHONKILSSVQAMRTOMQQMHGRMPVP 921
951 LARIGITAITHONKILSSVQAMRTOMQQMHGRMPVP 986

886 LARIGITAI THONKILSSVQAMRTOMQMHGRMPV 921
951 LARIGITAI THONKILSSVQAMRTOMQMHGRMPV 986

Fig. 16 (Cont.)

```

1 MNDFGIKNMDQVAPVANSYRGTLKRQPAFDTFDGS LFAVFP SLNEEQTLQ 50
  |||||
1 MNDFGIKNMDQVAPVANSYRGTLKRQPAFDTFDGS LFAVFP SLNEEQTLQ 50

51 EVPTGLDSISHDSANCELP LLTPCSKAVMSQALKA TFSGF..... 90
  |||||
51 EVPTGLDSISHDSANCELP LLTPCSKAVMSQALKA TFSGFKEQRR LGIP 100

91 .....FWATNEFSLVNVN LQRFGMNGQMLCN LGKERFLEL 125
  |||||
101 KNPWLWSEQQVCQWLLWATNEFSLVNVN LQRFGMNGQMLCN LGKERFLEL 150

126 APDFVGDILWEHLEQMIKENQEKTEDQYEENSHL TSVPHWINSNTLGF GT 175
  |||||
151 APDFVGDILWEHLEQMIKENQEKTEDQYEENSHL TSVPHWINSNTLGF GT 200

176 EQAPYGMQTQNYPKGGLLD SMCPASTPSVL SSEQEFQMF PKSLSSVSVT 225
  |||||
201 EQAPYGMQTQNYPKGGLLD SMCPASTPSVL SSEQEFQMF PKSLSSVSVT 250

226 YCSVSQDFPGSNLNL LTNNSGTPKDH DSPENGADSFESSDSL LQSWNSQS 275
  |||||
251 YCSVSQDFPGSNLNL LTNNSGTPKDH DSPENGADSFESSDSL LQSWNSQS 300

```

Fig. 17

276 SLVDVQRPVSFEFEDDCSCLNKPMTSEFKDYIQERSDPVEQKPVIP 325
 |||||
 301 SLVDVQRPVSFEFEDDCSCLNKPMTSEFKDYIQERSDPVEQKPVIP 350
 |||||
 326 AAVLAGFTGSGPIQLWQFLLLELLSDKSCQSFISWTGDGWEFKLADPDEVA 400
 |||||
 351 AAVLAGFTGSGPIQLWQFLLLELLSDKSCQSFISWTGDGWEFKLADPDEVA 425
 |||||
 376 RRWGKRKNKPKMNYEKLRLYYDKNIIHKTSRKRYVYRFVCDLQNL 450
 |||||
 401 RRWGKRKNKPKMNYEKLRLYYDKNIIHKTSRKRYVYRFVCDLQNL 450
 |||||
 426 GFTPEELHAILGVQPDTE 444
 |||||
 451 GFTPEELHAILGVQPDTE 469

Fig. 17 (Cont.)

```

1 MAGSAMSSKFFLVALAIFFSFAQVVEANSWWSLGMNPNVQMSEVYIIGA 50
  |||||
1 MAGSAMSSKFFLVALAIFFSFAQVVEANSWWSLGMNPNVQMSEVYIIGA 50

51 QPLCSQLAGLSQGQKKLCHLYQDHMQYIGEGAKTGIKECQYQFRHRRWNC 100
  |||||
51 QPLCSQLAGLSQGQKKLCHLYQDHMQYIGEGAKTGIKECQYQFRHRRWNC 100

101 STVDNTSVFGRVMQIGSRETAFTYAVSAAGVNVNAMSRACTEGELSTCGCS 150
  |||||
101 STVDNTSVFGRVMQIGSRETAFTYAVSAAGVNVNAMSRACTEGELSTCGCS 150

151 RAARPKDLPRDWLWGGCGDNIDYGYRFAKEFVDARERERIHAKGSYESAR 200
  |||||
151 RAARPKDLPRDWLWGGCGDNIDYGYRFAKEFVDARERERIHAKGSYESAR 200

201 ILMNLHNNAGRRRTVYNLADVACKCHGVSGCSLKTCLWLQLADFRKVGDA 250
  |||||
201 ILMNLHNNAGRRRTVYNLADVACKCHGVSGCSLKTCLWLQLADFRKVGDA 250

251 LKEKYDT 257
  |||||
251 LKEKYDS 257

```

Fig. 18

```

1 MALRRSMGRPGLPPLPLPPPPRLGLLLAESAAGLKLMGAPVKLTVSQGQ 50
  |||||
1 MALRRSMGRPGLPPLPLPPPPRLGLLLAESAAGLKLMGAPVKLTVSQGQ 50

51 PVKLNCSEGMEEPDIQWVKDGAVVQNLDQLYIPVSEQHWIGFSLKSVE 100
  |||||
51 PVKLNCSEGMEEPDIQWVKDGAVVQNLDQLYIPVSEQHWIGFSLKSVE 100

101 RSDAGRYWCQVEDGGETEISQPVWLTVEGVPEFTVEPKDLAVPPNAPFQL 150
  |||||
101 RSDAGRYWCQVEDGGETEISQPVWLTVEGVPEFTVEPKDLAVPPNAPFQL 150

151 SCEAVGPPEPVTIVVWRGTTKIGGPAPSPSVLNVGTQSTMFSCAHNL 200
  |||||
151 SCEAVGPPEPVTIVVWRGTTKIGGPAPSPSVLNVGTQSTMFSCAHNL 200

201 KGLASSRTATVHLQALPAAPFNI TVTKLSSNASVAVWMPGADGRALLQSC 250
  |||||
201 KGLASSRTATVHLQALPAAPFNI TVTKLSSNASVAVWMPGADGRALLQSC 250

251 TVQVTQAPGGWEVLAVVVPVPPFTCLLRDLVPATNYSLRVRCANALGPSP 300
  |||||
251 TVQVTQAPGGWEVLAVVVPVPPFTCLLRDLVPATNYSLRVRCANALGPSP 300

```

Fig. 19

```

301 YADWVPFQTKGLAPASAPQNLHAIRTDGLILEWEEVIPEAPLEGPLGPY 350
|||||
301 YADWVPFQTKGLAPASAPQNLHAIRTDGLILEWEEVIPEAPLEGPLGPY 350
|||||
301 YADWVPFQTKGLAPASAPQNLHAIRTDGLILEWEEVIPEAPLEGPLGPY 400
|||||
351 KLSWVQDNGTQDELTVETRANLTGWDPQKDLIVRVCVSNVAVGCGPWSQP 400
|||||
351 KLSWVQDNGTQDELTVETRANLTGWDPQKDLIVRVCVSNVAVGCGPWSQP 450
|||||
401 LVSSSHDRAGQQGPPHSRTSWVPVVLGVLTALVTAAALALILLRKRKKE 450
|||||
401 LVSSSHDRAGQQGPPHSRTSWVPVVLGVLTALVTAAALALILLRKRKKE 450
|||||
451 RFGQAFDSVMARGEPAVHFRAARSFNRPERPERIEATLDSLISDELKEKL 500
|||||
451 RFGQAFDSVMARGEPAVHFRAARSFNRPERPERIEATLDSLISDELKEKL 550
|||||
501 EDVLIPEQQFTLGRMLGKGEFGSVREAQKQEDGSFVKVAVKMLKADIIA 550
|||||
501 EDVLIPEQQFTLGRMLGKGEFGSVREAQKQEDGSFVKVAVKMLKADIIA 600
|||||
551 SSDIEEFFLREAAACMKKEFDHPHVAKLVGVSLRSRAKGRLLPIMVILPFMKH 600
|||||
551 SSDIEEFFLREAAACMKKEFDHPHVAKLVGVSLRSRAKGRLLPIMVILPFMKH 600

```

Fig. 19 (Cont.)

601 GDLHAFLLASRIGENPFNLPLQTLIRFMVVDIACGMEYLSRNFIHRDLAA 650
 |||||
 601 GDLHAFLLASRIGENPFNLPLQTLIRFMVVDIACGMEYLSRNFIHRDLAA 650

651 RNCMLAEDMTVCVADFGLSRKIYSDCRY 678
 |||||
 651 RNCMLAEDMTVCVADFGLSRKIYSGDYY 678

Fig. 19 (Cont.)

Fig. 20

```

301 NGMLRYRIVSQAPSTPSPNMFNNETGDIITVAAGLDREKVQQTLLIQ 350
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 NGMLRYRIVSQAPSTPSPNMFNNETGDIITVAAGLDREKVQQTLLIQ 350

   . . .
351 ATDMEGNPTYGLSNTATAVITVDVNDNPPEFTAMTFYGEVPEENRVDIIV 400
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
351 ATDMEGNPTYGLSNTATAVITVDVNDNPPEFTAMTFYGEVPEENRVDIIV 400

   . . .
401 ANLTVTDKQDQHTPAWNAVYRISGGDPTGRFAIQTDPNNSNDGLVTVKPI 450
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
401 ANLTVTDKQDQHTPAWNAVYRISGGDPTGRFAIQTDPNNSNDGLVTVKPI 450

   . . .
451 DFETNRMFVLTVAAEQVPLAKGIQHPPQSTATVSVTVIDVNNENPYFAPN 500
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
451 DFETNRMFVLTVAAEQVPLAKGIQHPPQSTATVSVTVIDVNNENPYFAPN 500

   . . .
501 PKIIRQEEGLHAGTMLTTFTAQDPPDRYMQQNIRYTKLSDPANWLKIDPVN 550
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
501 PKIIRQEEGLHAGTMLTTFTAQDPPDRYMQQNIRYTKLSDPANWLKIDPVN 550

   . . .
551 GQITTI AVLDR ESPNVKNNIYNATFLASDNGIPPM SGTGT LQIYLLDIND 600
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
551 GQITTI AVLDR ESPNVKNNIYNATFLASDNGIPPM SGTGT LQIYLLDIND 600

```

Fig. 20 (Cont.)

```

601  NAPQVLPQEAETCETPDPSINITALDYDIDPNAGPFAFDLPLSPVTIKR 650
      |||||
601  NAPQVLPQEAETCETPDPSINITALDYDIDPNAGPFAFDLPLSPVTIKR 650

651  NWTITRLNGDFAQLNLKIKFLEAGIYEVPIIITDSGNPPKSNISILRVKV 700
      |||||
651  NWTITRLNGDFAQLNLKIKFLEAGIYEVPIIITDSGNPPKSNISILRVKV 700

701  CQCDNSGDCSTDVDRIVGAGLGTGAIIAILLIILVLMFVVMKRRD 750
      |||||
701  CQCDNSGDCSTDVDRIVGAGLGTGAIIAILLIILVLMFVVMKRRD 750

751  KERQAKQLLIDPEDDVRDNILKYDEEGGEEDQDYDLSQLQQPDTVEPDA 800
      |||||
751  KERQAKQLLIDPEDDVRDNILKYDEEGGEEDQDYDLSQLQQPDTVEPDA 800

      801  IKPVGIRRMDERPIHAEPQYPVRSAAAPHGDIGDFINE 838
          |||||
      801  IKPVGIRRMDERPIHAEPQYPVRSAAAPHGDIGDFINE 838

```

Fig. 20 (Cont.)

1 MERVKMINVQRLLEAAEFLERRERECEHGYASSFPMPSPRLOHSKPPRR 50
| | | | | | | | | | | | | | | | | | | | | | | | | |
1 MERVKMINVQRLLEAAEFLERRERECEHGYASSFPMPSPRLOHSKPPRR 50

51 LSRAQKHSSGSSNTSTANRSTHNELEKNR 79
 ||||| . ||||| ||||| ||||| |||||
 51 LSRAQKHSSGTSNTSTANRSTHNELEKNR 79

Fig. 21

```

11 NVQILLEAASYLEQIEKENKKCEHGYASSFPSPRLQHSKPPRRLSRA 60
   ||| |||| :||. |:|| ||||| ||||| ||||| ||||| |||||
8 NVQRLLEAAEFFLERRERE...CEHGYASSFPSPRLQHSKPPRRLSRA 54

61 QKHSSGSSNTSTANRSTHNELEKNRRRAHLRLCLERLKVLIPLGPDCTRHT 110
   |||||. ||||| ||||| ||||| ||||| ||||| ||||| |||||
55 QKHSSGTSNTSTANRSTHNELEKNRRRAHLRLCLERLKVLIPLGPDCTRHT 104

111 TLGLLNKAKAHIKKLEEAERKSQHOLENLEREQRFLKWRLEQLQGPQEME 160
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
105 TLGLLNKAKAHIKKLEEAERKSQHOLENLEREQRFLKWRLEQLQGPQEME 154

161 RIRMDSIGSTISSDRSDSEREEIEVDVESTEFESHGEVDNISTSIDIDD 210
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
155 RIRMDSIGSTISSDRSDSEREEIEVDVESTEFESHGEVDNISTSIDIDD 204

211 HSSLPSIGSDEGYSSASVKLSFTS 234
   ||||| ||||| ||||| ||||| |||||
205 HSSLPSIGSDEGYSSASVKLSFTS 228

```

Fig. 22

1 MESPASSQPASMPQSKGSKRKKDLRISCMSPKPPAPNPTPPRNLDSTFI 50
 |||||
 1 MESPASSQPASMPQSKGSKRKKDLRISCMSPKPPAPNPTPPRNLDSTFI 50

51 TIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVKRIRATVN 100
 |||||
 51 TIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVKRIRATVN 100

101 SEQQRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKF 150
 |||||
 101 SEQQRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKF 150

151 YRKVLDKNMTIPEDILGEIAVSIVRALEHLHSLKLSVIHRDVKPSNVLINK 200
 |||||
 151 YRKVLDKNMTIPEDILGEIAVSIVRALEHLHSLKLSVIHRDVKPSNVLINK 200

201 EGHVKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSD 250
 |||||
 201 EGHVKMCDFGISGYLVDSVAKTMDAGCKPYMAPERINPELNQKGYNVKSD 250

Fig. 23

251 VWSLGITMIEMAILRFPYESWGTFPQQLKQVVEEPSQLPADRFSPFVD 300
 |||||
 251 VWSLGITMIEMAILRFPYESWGTFPQQLKQVVEEPSQLPADRFSPFVD 300

301 FTAQCLRKKNPAERMSYLELI 320
 |||||
 301 FTAQCLRKKNPAERMSYLELM 320

Fig. 23(Cont.)

```

1 MPEIRLRHVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISVVLQLE 50
  |||||
1 MPEIRLRHVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISVVLQLE 50

51 KEEQIHSVDIGNDGSFAFVEVLVGSSAGGAGEQDYEVLLVTSFMSPPESR 100
  |||||
51 KEEQIHSVDIGNDGSFAFVEVLVGSSAGGAGEQDYEVLLVTSFMSPPESR 100

101 SGSNPNRVRMFGPDKLVRAAAEKRWDVRKIVCSQPYSKDSPFGLSFVRFH 150
  |||||
101 SGSNPNRVRMFGPDKLVRAAAEKRWDVRKIVCSQPYSKDSPFGLSFVRFH 150

151 SPDDKDEAEAPSQKVTVTKLQGFVRVKEEDEANSLRPGALFFSRINKTSP 200
  |||||
151 SPDDKDEAEAPSQKVTVTKLQGFVRVKEEDEANSLRPGALFFSRINKTSP 200

201 VTASDPAGPSYAAATLQASSAASSASPVSRAIGSTSKPQESP 242
  |||||
201 VTASDPAGPSYAAATLQASSAASSASPVSRAIGSTSKPQESP 242

```

Fig. 24

Fig. 25

```

1 MPEIRLRHVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISVVLQLE 50
  |||||
1 MPEIRLRHVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISVVLQLE 50
  |||||
51 KEEQIHSVDIGNDGSFVEVLVGSSAGGAGEQDYEVLLVTSFMSPSES 100
  |||||
51 KEEQIHSVDIGNDGSFVEVLVGSSAGGAGEQDYEVLLVTSFMSPSES 100
  |||||
101 SGSNPNRVRMFGPDKLVRAAAEKRWDVRKIVCSQPYSKDSPFGLSFVRFH 150
  |||||
101 SGSNPNRVRMFGPDKLVRAAAEKRWDVRKIVCSQPYSKDSPFGLSFVRFH 150
  |||||
151 SPPDKDEAEAPSQKVTVTKLGQFRVKEEDESANSLRLEDYMSDRVQFV.. 198
  |||||
151 SPPDKDEAEAPSQKVTVTKLGQFRVKEEDESANSLRPGALFFSRINKTSP 200
  |||||
199 ITAQE.WDPSEEEALMDNP SLA 219
  :||: ||: |: |: |
201 VTASDPAGPSYAAATLQASSAA 222

```

Fig. 26

1 MPEIRLRHVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISVVLQLE 50
 |||||
 1 MPEIRLRHVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISVVLQLE 50
 51 KEEQIHSVDIGNDGS AFVEVL VGSSAGGAGEQDYEVLLVTSSFMSPSESR 100
 |||||
 51 KEEQIHSVDIGNDGS AFVEVL VGSSAGGAGEQDYEVLLVTSSFMSPSESR 100
 101 SGSNPNVRMEFGPDKLVRAAAEKRWDVRKIVCSQPYSKDSPFGLSFVRFH 150
 |||||
 101 SGSNPNVRMEFGPDKLVRAAAEKRWDVRKIVCSQPYSKDSPFGLSFVRFH 150
 151 SPDPKDEAEAPSQKVTVTKLGQFRVKEEDESANSLRPGALFFSRINKTSP 200
 |||||
 151 SPDPKDEAEAPSQKVTVTKLGQFRVKEEDESANSLRPGALFFSRINKTSP 200
 201 VTASDPAGPSYAAATLQASSAASSASPVSRAIGSTSKPQESPCKGRKKLDL 250
 |||||
 201 VTASDPAGPSYAAATLQASSAASSASPVSRAIGSTSKPQESPCKGRKKLDL 250
 251 NQEEKKTPSKPPAQLSPSPVKRPKLPAPTRTPATAPVPARAQGAVTGKPR 300
 |||||
 251 NQEEKKTPSKPPAQLSPSPVKRPKLPAPTRTPATAPVPARAQGAVTGKPR 300

Fig. 27

301	GEGTEPRRPRAGPEELGKILQGVVVLSGFQNPFRSEL	RDKALELGAKYR	350
301	GEGTEPRRPRAGPEELGKILQGVVVLSGFQNPFRSEL	RDKALELGAKYR	350
351	PDWTRDSTHLICAFANTPKYSQVLGLGGRIVRK	EWVLDCHRMRRRLPSRR	400
351	PDWTRDSTHLICAFANTPKYSQVLGLGGRIVRK	EWVLDCHRMRRRLPSRR	400
401	YLMAGPGSSSEDEASHSGSGDEAPKLPQKQPQTKTKPTQAAGPSSPQK		450
401	YLMAGPGSSSEDEASHSGSGDEAPKLPQKQPQTKTKPTQAAGPSSPQK		450
451	PPTPEETKAASPVLQEDIDIEGVQSEGQDNGAEDSGDTEDELRRVAEQKE		500
451	PPTPEETKAASPVLQEDIDIEGVQSEGQDNGAEDSGDTEDELRRVAEQKE		500
501	HRLPQGQEEGEDPYAGSTDENTDSEEHQEPDLPVPELPRFLPGQ		546
501	HRLPQGQEEGEDPYAGSTDENTDSEEHQEPDLPVPELPRFLPGQ		546

Fig. 27(Cont.)

1 MAGAIASRMSFSSLLKRPQKFTTVRIVTMDAEMEFNCMKWKGDLEFLV 50
 |||||
 1 MAGAIASRMSFSSLLKRPQKFTTVRIVTMDAEMEFNCMKWKGDLEFLV 50
 51 CRTGLRETWFFGLQYTIKDTVAWLKMDKKVLDHVDVSKEEPTVFHFLAKF 100
 |||||
 51 CRTGLRETWFFGLQYTIKDTVAWLKMDKKVLDHVDVSKEEPTVFHFLAKF 100
 101 YPENAEELVQEITQHLFFLQVKKQILDDEKIYCPPEASVLLASYAVQAKY 150
 |||||
 101 YPENAEELVQEITQHLFFLQVKKQILDDEKIYCPPEASVLLASYAVQAKY 150
 151 GDYDPSVHKRGFLAQEELLPKRVINLYQMTPEMWEERITAWYAEHRGRAR 200
 |||||
 151 GDYDPSVHKRGFLAQEELLPKRVINLYQMTPEMWEERITAWYAEHRGRAR 200
 201 DEAEEMEYLKIAQDLEMYGVNYFAIRNKKGTLELLGVDAIGLHIYDPENRL 250
 |||||
 201 DEAEEMEYLKIAQDLEMYGVNYFAIRNKKGTLELLGVDAIGLHIYDPENRL 250
 251 TPKISFPWKNEIRNISYSKDEFTIKPLDKKIDVFKFNSSKLVRNKLILQL 300
 |||||
 251 TPKISFPW.NEIRNISYSKDEFTIKPLDKKIDVFKFNSSKLVRNKLILQL 299

Fig. 28

301 CIGNHDLFMRRRKADSLVQMQKAQAREEKARK..... 333
 |||||
 300 CIGNHDLFMRRRKADSLVQMQKAQAREEKARKOMERQRLAREKQMREEA 349
 334QMKEEATMANEALMRSEETADLLAEKAQITEEEAKLLA 371
 |||||
 350 ERTRDELERLLQMKEEATMANEALMRSEETADLLAEKAQITEEEAKLLA 399
 372 QKAAEAQEMQRIKATAIRTEEEKRLMEQKVLAEVLAALKMAEESERRAK 421
 |||||
 400 QKAAEAQEMQRIKATAIRTEEEKRLMEQKVLAEVLAALKMAEESERRAK 449
 422 EADQLKQDLQEAAREARRAKQKLLIATKPTYPMPNPIAPLPPDIPSN 471
 |||||
 450 EADQLKQDLQEAAREARRAKQKLLIATKPTYPMPNPIAPLPPDIPSN 499
 472 LIGDSLSEDFKDTDMKRLSMEIEKEKVEYMEKSKHLQEQNLKTEIEAL 521
 |||||
 500 LIGDSLSEDFKDTDMKRLSMEIEKEKVEYMEKSKHLQEQNLKTEIEAL 549
 522 KLKERETALDILHNENSDRGSSKHNTIKKLTQSAKSRVAFFEEEL 567
 |||||
 550 KLKERETALDILHNENSDRGSSKHNTIKKLTQSAKSRVAFFEEEL 595

Fig. 28 (Cont.)

```

1 MRERFDRFLHEKNCMTDLLAKLEAKTGVNRSFIALGVIGLVALYLVFGYG 50
  |||||
1 MRERFDRFLHEKNCMTDLLAKLEAKTGVNRSFIALGVIGLVALYLVFGYG 50
  |||||
51 ASLLCNLIGFGYPAYISIKAIESPNKEDDTQWLTYWVVYGVFSIAEFFSD 100
  |||||
51 ASLLCNLIGFGYPAYISIKAIESPNKEDDTQWLTYWVVYGVFSIAEFFSD 100
  |||||
  101 IFLSWFFPYMYMLK 113
    |||||
  101 IFLSWFFPYMYMLK 113

```

Fig. 29

```

1 MDLEGRNGGAKKKNFFKLNKSEKDKKEKPTVSFMSFRYSNWLDKLY 50
  |||||
1 MDLEGRNGGAKKKNFFKLNKSEKDKKEKPTVSFMSFRYSNWLDKLY 50

51 MVVGTAAIITHGAGLPLMMLVFGEMTDIFANAGNLEDLMSNITNRSIND 100
  |||||
51 MVVGTAAIITHGAGLPLMMLVFGEMTDIFANAGNLEDLMSNITNRSIND 100

101 TGFFMNLEEDMTRYAYYYSGIGAGVLVAAYIQVSFWCLAAGRQIHKIRKQ 150
  |||||
101 TGFFMNLEEDMTRYAYYYSGIGAGVLVAAYIQVSFWCLAAGRQIHKIRKQ 150

151 FFHAIMRQEIIGWFDVHDVGELNTRLTDDVSKINEVIGDKIGMFFQSMATF 200
  |||||
151 FFHAIMRQEIIGWFDVHDVGELNTRLTDDVSKINEVIGDKIGMFFQSMATF 200

201 FTGFI VGTFRGWKLTIVILAI SPVLGLSAAVWAKILSSFTDKELLAYAKA 250
  |||||
201 FTGFI VGTFRGWKLTIVILAI SPVLGLSAAVWAKILSSFTDKELLAYAKA 250

251 GAVAEVLA AIRT VIAFGGQKKELE RYNKNLEEA KRIGIKKAITANISIG 300
  |||||
251 GAVAEVLA AIRT VIAFGGQKKELE RYNKNLEEA KRIGIKKAITANISIG 300

```

Fig. 30


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301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQVLTFFSVLIGAFSVGQASP 350
|||||
301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQVLTFFSVLIGAFSVGQASP 350

351 SIEAFANARGAAYEIFKIIDNKPIDSYSKSGHKPDNIKGNLEFRNVHFS 400
|||||
351 SIEAFANARGAAYEIFKIIDNKPIDSYSKSGHKPDNIKGNLEFRNVHFS 400

401 YPSRKEVKILKGLNLKVQSGQTVALVNSGCCGKSTTVQLMQRLYDPTGEM 450
|||||
401 YPSRKEVKILKGLNLKVQSGQTVALVNSGCCGKSTTVQLMQRLYDPTGEM 450

451 VSVDGQDIRTINVRFLREIIGVVSQEPVLEATTIAENIRYGRENVMTDEI 500
|||||
451 VSVDGQDIRTINVRFLREIIGVVSQEPVLEATTIAENIRYGRENVMTDEI 500

501 EKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIARALVRNPK 550
|||||
501 EKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIARALVRNPK 550

551 ILLDEATSALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
|||||
551 ILLDEATSALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600

```

Fig. 30 (Cont.)

901 IENFRTVVSILTQEQKFEHMYAQSLQVYRNSLRKAHIFGITSFTQAMMY 950
 |||||
 901 IENFRTVVSILTQEQKFEHMYAQSLQVYRNSLRKAHIFGITSFTQAMMY 950
 .
 951 FSYAGCFRFGAYLVAHKIMSFEDVLLVFSVFGAMAVGQVSSFAPDYAK 1000
 |||||
 951 FSYAGCFRFGAYLVAHKIMSFEDVLLVFSVFGAMAVGQVSSFAPDYAK 1000
 .
 1001 AKISAAHIIMIEKTPLIDSYSTEGMLPNTLEGNVTFGEVVFNYPTRPDI 1050
 |||||
 1001 AKISAAHIIMIEKTPLIDSYSTEGMLPNTLEGNVTFGEVVFNYPTRPDI 1050
 .
 1051 PVLQGLSLEVKKGQTLALVGSSGCGKSTVVQLLERYDPLAGKVLLDGKE 1100
 |||||
 1051 PVLQGLSLEVKKGQTLALVGSSGCGKSTVVQLLERYDPLAGKVLLDGKE 1100
 .
 1101 IKRLNVQWLRAHLGIVSQEPILFDCSIAENIAYGDNRSRVVSQEEIVRAAK 1150
 |||||
 1101 IKRLNVQWLRAHLGIVSQEPILFDCSIAENIAYGDNRSRVVSQEEIVRAAK 1150
 .
 1151 EANIHAFTESLPNKYSTKVGDKGTLQSLGGQKQRIARALVRQPHILLD 1200
 |||||
 1151 EANIHAFTESLPNKYSTKVGDKGTLQSLGGQKQRIARALVRQPHILLD 1200

1201	EATSALDTESEKVVQEALDKAREGRTTCIVIAHRLSTIQNADLIVVFQNGR	1250
1201	EATSALDTESEKVVQEALDKAREGRTTCIVIAHRLSTIQNADLIVVFQNGR	1250
	1251 VKEHGTHQQLLAQKGIYFSMVSQAGT	1277
	1251 VKEHGTHQQLLAQKGIYFSMVSQAGT	1277

Fig. 30(Cont.)

1 MDLEGDRNGGAKKKNFKLNKSEKDKKKKPTVSFMSFRYSNWLDKLY 50
 |||||
 1 MDLEGDRNGGAKKKNFKLNKSEKDKKKKPTVSFMSFRYSNWLDKLY 50

51 MVVGTAAIIHGAGLPLMLVFGEMTDIFANAGNLEDLMSNITNRSND 100
 |||||
 51 MVVGTAAIIHGAGLPLMLVFGEMTDIFANAGNLEDLMSNITNRSND 100

101 TGEFMNLEEDMTRYAYYYSGIGAGVLVAAYIQVSFWCLAAGRQIHKIRKQ 150
 |||||
 101 TGEFMNLEEDMTRYAYYYSGIGAGVLVAAYIQVSFWCLAAGRQIHKIRKQ 150

151 FFHAIMRQEIGWFDVHDVGELNTRLTDDVSKINEGIGDKIGMFFQSMATF 200
 |||||
 151 FFHAIMRQEIGWFDVHDVGELNTRLTDDVSKINEVIGDKIGMFFQSMATF 200

201 FTGEIVGFTTRGWKLTLLVLAISPVLGLSAAVWAKILSSFTDKELLAYAKA 250
 |||||
 201 FTGEIVGFTTRGWKLTLLVLAISPVLGLSAAVWAKILSSFTDKELLAYAKA 250

251 GAVAEVLAIRTVIAFGGQKKELERYKNKNLEEAKRIGIKKAITANISIG 300
 |||||
 251 GAVAEVLAIRTVIAFGGQKKELERYKNKNLEEAKRIGIKKAITANISIG 300

Fig. 31

```

301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQVLTFFSVLIGAFSVGQASP 350
|||||
301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQVLTFFSVLIGAFSVGQASP 350
|||||

351 SIEAFANARGAAEIFKIIDNKPSIDSYSGHKGPDNIKGNLEFRNVHFS 400
|||||
351 SIEAFANARGAAEIFKIIDNKPSIDSYSGHKGPDNIKGNLEFRNVHFS 400
|||||

401 YPSRKEVKILKGLNLKVQSGQTVALVGNSGCGKSTTVQLMQRLYDPTEGM 450
|||||
401 YPSRKEVKILKGLNLKVQSGQTVALVGNSGCGKSTTVQLMQRLYDPTEGM 450
|||||

451 VSVDGQDIRTINVRFLREIIGVVSQEPVLFATTIAENIRYGRENVMTDEI 500
|||||
451 VSVDGQDIRTINVRFLREIIGVVSQEPVLFATTIAENIRYGRENVMTDEI 500
|||||

501 EKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIAIARALVRNPK 550
|||||
501 EKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKQRIAIARALVRNPK 550
|||||

551 ILLLDEATSALDTESEAEVQAALDKVSR 578
|||||
551 ILLLDEATSALDTESEAVVQVALDKARK 578

```

Fig. 31(Cont.)

1 MSRSKRDNNFYSVEIGDSTFTVLKRYQNLKPIGSAQGIVCAAYDAILER 50
| | | | | | | | | | | | | | | | | | | | | | | | | |
1 MSRSKRDNNFYSVEIGDSTFTVLKRYQNLKPIGSAQGIVCAAYDAILER 50

51 NVAIKKLSRPFQNTAHAKRAYRELVMKC VNHNKI IGLLNVFTPQSLEE 100
| | | | | | | | | | | | | | | | | | | | | | | | | |
51 NVAIKKLSRPFQNTAHAKRAYRELVMKC VNHNKI IGLLNVFTPQSLEE 100

101 FQDVYI VMELMDANLCQVIQMELDHHERMSYLLYQMLCGIKHLHSAGIIHR 150
| | | | | | | | | | | | | | | | | | | | | | | | | |
101 FQDVYI VMELMDANLCQVIQMELDHHERMSYLLYQMLCGIKHLHSAGIIHR 150

151 DLKPSNIVVKS DCTLKILDFGLARTAGTSFMMTPYVVTRYRAPEVILGM 200
| | | | | | | | | | | | | | | | | | | | | | | | | |
151 DLKPSNIVVKS DCTLKILDFGLARTAGTSFMMTPYVVTRYRAPEVILGM 200

201 GYKENTE 207
| | | | :
201 GYKENVD 207

Fig. 32

1 MSRSKRDNNFYSVEIGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAILER 50
 |||||
 1 MSRSKRDNNFYSVEIGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAILER 50

51 NVAIKKLSRPFQNOHAKRAYRELVLKMCVNHKNIIGLLNVFTPQKSLEE 100
 |||||
 51 NVAIKKLSRPFQNOHAKRAYRELVLKMCVNHKNIIGLLNVFTPQKSLEE 100

101 FQDVYIVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIIHR 150
 |||||
 101 FQDVYIVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIIHR 150

151 DLKPSNIVVKS DCTLKILDFGLARTAGTSEFMMTPYVVTRYRAPEVILGM 200
 |||||
 151 DLKPSNIVVKS DCTLKILDFGLARTAGTSEFMMTPYVVTRYRAPEVILGM 200

201 GYKENVDLWSVGCIMGEMVCHKILFPGRDYIDQWNKVIEQLGTPCPEFMK 250
 |||||
 201 GYKENVDLWSVGCIMGEMVCHKILFPGRDYIDQWNKVIEQLGTPCPEFMK 250

251 KLOPTVRTYVENRPKYAGYSFEKLFPPDVLFPADSEHNKCLKASQ 293
 |||||
 251 KLOPTVRTYVENRPKYAGYSFEKLFPPDVLFPADSEHNKCLKASQ 293

Fig. 33


```

251 KLQPTVRTYVENRPPKYAGYSFEKLPDVLFPADSEHNKCLKASQARDLLSK 300
|||||
251 KLQPTVRTYVENRPPKYAGYSFEKLPDVLFPADSEHNKCLKASQARDLLSK 300

301 MLVIDASKRISVDEALQHPYINVWYDPSEAEARSCKL 337
|||||
301 MLVIDASKRISVDEALQHPYINVWYDPSEAEAPPKI 337

```

Fig. 34(Cont.)

7 arsgfyrqevtktawevravryrdlqpvgsgaygavcsavdgrtgakvaik 56
 |||||
 1 ARSGFYRQEVTKTAWEVRAVRYRDLQPVGSGAYGAVCSAVDGRGTGAKVAIK 50
 57 klyrpfqsselfakrayrelrlklkhrhenviglldvftpdetlddftdfy 106
 |||||
 51 KLYRPFQSELF AKRAYRELRLKLKMRHENVIGLLDVFTPDETLDDFTDFY 100
 107 lvmpfmgtdlgklmkheklgedriqlvyqmlkglyrihaagiihrdlkp 156
 |||||
 101 LVMPFMGTDLGKLMKHEKLGEDRIQFLVYQMLKGLRYIHAAGIIHR.VSP 149
 157 gnlavne 163
 |||
 150 GGEAAHQ 156

Fig. 35

```

1 MSPFLRIGLSNFDGSCQSGEAVNPYCAVLVKEYVESENGQMYIQKP 50
  |||||
1 MSPFLRIGLSNFDGSCQSGEAVNPYCAVLVKEYVESENGQMYIQKP 50

51 TYPWPWDSTFDAHINKGRVMQIIVKGNVDLISSETVELYSLAERCERN 100
  |||||
51 TYPWPWDSTFDAHINKGRVMQIIVKGNVDLISSETVELYSLAERCERN 100

101 GKTEIWLELKPQGRMLMNARYFLEMSDTKDMNEFEFEGFFALHQRRAIK 150
  |||||
101 GKTEIWLELKPQGRMLMNARYFLEMSDTKDMNEFEFEGFFALHQRRAIK 150

151 QAKVHHVKCHEFTATFFPQPTFCVCHFEVWGLNKQGYQCRQCNAAIHKK 200
  |||||
151 QAKVHHVKCHEFTATFFPQPTFCVCHFEVWGLNKQGYQCRQCNAAIHKK 200

201 CIDKVIKCTGSAINSRETMFHKERFKIDMPHRFKVYNYKSPTFCEHCGT 250
  |||||
201 CIDKVIKCTGSAINSRETMFHKERFKIDMPHRFKVYNYKSPTFCEHCGT 250

```

Fig. 36

```

251 LLWGLARQGLKCDACGMNVHRCQTKVANLCGINQKLMAEALAMISTQQ 300
|||||
251 LLWGLARQGLKCDACGMNVHRCQTKVANLCGINQKLMAEALAMISTQQ 300

301 ARCLRDTEQIFREGPVEIGLPCSIKNEARPPCLTPGKREPQGISWESPL 350
|||||
301 ARCLRDTEQIFREGPVEIGLPCSIKNEARLPCLTPGKREPQGISWESPL 350

351 DEVDKMCHLPEPELNKERPSLQIKLKIEDFILHKMLGKSGFKVFLAEFK 400
|||||
351 DEVDKMCHLPEPELNKERPSLQIKLKIEDFILHKMLGKSGFKVFLAEFK 400

401 KTNQFFAIKALKKDVVLMDDDDVECTMVEKRVLSLAWEHPFLTHMECTFQT 450
|||||
401 KTNQFFAIKALKKDVVLMDDDDVECTMVEKRVLSLAWEHPFLTHMECTFQT 450

451 KENLFFVMEYLNCGDLMYHIQSCHKFDLSRATFYAAEIIILGLQFLHSGKI 500
|||||
451 KENLFFVMEYLNCGDLMYHIQSCHKFDLSRATFYAAEIIILGLQFLHSGKI 500

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Fig. 36 (Cont.)

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501 VYRDLKLDNILLDKDGHIKIADFGMCKENMLGDAKTNTFCGTPDYIAPEI 550
    |||||
501 VYRDLKLDNILLDKDGHIKIADFGMCKENMLGDAKTNTFCGTPDYIAPEI 550

551 LLGQKYNHSVDWWSFGVLLYEMLIQSPFHGQDEEEELFHSIRMDNPFYPR 600
    |||||
551 LLGQKYNHSVDWWSFGVLLYEMLIQSPFHGQDEEEELFHSIRMDNPFYPR 600

601 WLEKEAKDLLVK..VRSEAKSVFIR 623
    |||||
601 WLEKEAKDLLVKLFVREPEKRLGVR 625

```

Fig. 36 (Cont.)